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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/756,071B

DATE: 08/17/2001
TIME: 14:25:18

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\08172001\I756071B.raw

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Tryggvason, Karl
6 Kallunki, Pekka
7 Pyke, Charles
9 (ii) TITLE OF INVENTION: Laminin Chains: Diagnostic Uses
11 (iii) NUMBER OF SEQUENCES: 20
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Fay Sharpe Fagan Minnich & McKee
15 (B) STREET: 1100 Superior Ave, Suite 700
16 (C) CITY: Cleveland
17 (D) STATE: Ohio
18 (E) COUNTRY: USA
19 (F) ZIP: 44114
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/756,071B
C--> 29 (B) FILING DATE: 08-Jan-2001
35 (C) CLASSIFICATION:
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: US 09/663,147
34 (B) FILING DATE: 150-September 2000
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Minnich, Richard, J.
39 (B) REGISTRATION NUMBER: 24,175
40 (C) REFERENCE/DOCKET NUMBER: TRV 20014
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 216-861-5582
44 (B) TELEFAX: 216-241-1666
46 (2) INFORMATION FOR SEQ ID NO: 1:
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 20 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: single
52 (D) TOPOLOGY: linear
54 (ii) MOLECULE TYPE: other nucleic acid
55 (A) DESCRIPTION: /desc = "oligomer primers"
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
59 GGCTCACCAA GACTTACACA
61 (2) INFORMATION FOR SEQ ID NO: 2:
63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 20 base pairs
65 (B) TYPE: nucleic acid

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66 (C) STRANDEDNESS: single
 67 (D) TOPOLOGY: linear
 69 (ii) MOLECULE TYPE: other nucleic acid
 70 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
 72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 74 GAATCACTGA GCAGCTGAAC 20
 76 (2) INFORMATION FOR SEQ ID NO: 3:
 78 (i) SEQUENCE CHARACTERISTICS:
 79 (A) LENGTH: 20 base pairs
 80 (B) TYPE: nucleic acid
 81 (C) STRANDEDNESS: single
 82 (D) TOPOLOGY: linear
 84 (ii) MOLECULE TYPE: other nucleic acid
 85 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
 87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 89 CAGTACCGAG ACCGAGTTCG 20
 91 (2) INFORMATION FOR SEQ ID NO: 4:
 93 (i) SEQUENCE CHARACTERISTICS:
 94 (A) LENGTH: 20 base pairs
 95 (B) TYPE: nucleic acid
 96 (C) STRANDEDNESS: single
 97 (D) TOPOLOGY: linear
 99 (ii) MOLECULE TYPE: other nucleic acid
 100 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
 102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 104 CTGGTTACCA GGCTTGAGAG 20
 106 (2) INFORMATION FOR SEQ ID NO: 5:
 108 (i) SEQUENCE CHARACTERISTICS:
 109 (A) LENGTH: 20 base pairs
 110 (B) TYPE: nucleic acid
 111 (C) STRANDEDNESS: single
 112 (D) TOPOLOGY: linear
 114 (ii) MOLECULE TYPE: other nucleic acid
 115 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
 117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 119 TTACTGCGGA ATCTCACAGC 20
 121 (2) INFORMATION FOR SEQ ID NO: 6:
 123 (i) SEQUENCE CHARACTERISTICS:
 124 (A) LENGTH: 20 base pairs
 125 (B) TYPE: nucleic acid
 126 (C) STRANDEDNESS: single
 127 (D) TOPOLOGY: linear
 129 (ii) MOLECULE TYPE: other nucleic acid
 130 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
 132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 134 TACACTGTTC AACCCAGGGT 20
 136 (2) INFORMATION FOR SEQ ID NO: 7:
 138 (i) SEQUENCE CHARACTERISTICS:
 139 (A) LENGTH: 20 base pairs

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140 (B) TYPE: nucleic acid
141 (C) STRANDEDNESS: single
142 (D) TOPOLOGY: linear
144 (ii) MOLECULE TYPE: other nucleic acid
145 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
149 AAACAAAGCCCC TCTCACTGGT 20
151 (2) INFORMATION FOR SEQ ID NO: 8:
153 (i) SEQUENCE CHARACTERISTICS:
154 (A) LENGTH: 20 base pairs
155 (B) TYPE: nucleic acid
156 (C) STRANDEDNESS: single
157 (D) TOPOLOGY: linear
159 (ii) MOLECULE TYPE: other nucleic acid
160 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
164 GCGGAGACTG TGCTGATAAG 20
166 (2) INFORMATION FOR SEQ ID NO: 9:
168 (i) SEQUENCE CHARACTERISTICS:
169 (A) LENGTH: 20 base pairs
170 (B) TYPE: nucleic acid
171 (C) STRANDEDNESS: single
172 (D) TOPOLOGY: linear
174 (ii) MOLECULE TYPE: other nucleic acid
175 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
179 CATAACCTCTC TACATGGCAT 20
181 (2) INFORMATION FOR SEQ ID NO: 10:
183 (i) SEQUENCE CHARACTERISTICS:
184 (A) LENGTH: 20 base pairs
185 (B) TYPE: nucleic acid
186 (C) STRANDEDNESS: single
187 (D) TOPOLOGY: linear
189 (ii) MOLECULE TYPE: other nucleic acid
190 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
194 AGTCTCGCTG AATCTCTCTT 20
196 (2) INFORMATION FOR SEQ ID NO: 11:
198 (i) SEQUENCE CHARACTERISTICS:
199 (A) LENGTH: 20 base pairs
200 (B) TYPE: nucleic acid
201 (C) STRANDEDNESS: single
202 (D) TOPOLOGY: linear
204 (ii) MOLECULE TYPE: other nucleic acid
205 (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"
208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
210 TTACAACTAG CATGGTCCCC 20
212 (2) INFORMATION FOR SEQ ID NO: 12:
214 (i) SEQUENCE CHARACTERISTICS:

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215 (A) LENGTH: 5200 base pairs
 216 (B) TYPE: nucleic acid
 217 (C) STRANDEDNESS: single
 218 (D) TOPOLOGY: linear
 220 (ii) MOLECULE TYPE: cDNA
 223 (ix) FEATURE:
 224 (A) NAME/KEY: sig_peptide
 225 (B) LOCATION: 118..183
 227 (ix) FEATURE:
 228 (A) NAME/KEY: CDS
 229 (B) LOCATION: 118..3699
 231 (ix) FEATURE:
 232 (A) NAME/KEY: polyA_site
 233 (B) LOCATION: 4433
 235 (ix) FEATURE:
 236 (A) NAME/KEY: polyA_site
 237 (B) LOCATION: 5195
 240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 242 GACCACCTGA TCGAAGGAAA AGGAAGGCAC AGCGGAGCGC AGAGTGAGAA CCACCAACCG 60
 244 AGGCGCCGGG CAGCGACCCC TGCAGCGGAG ACAGAGACTG AGCGGCCCGG CACCGCC 117
 246 ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG 165
 247 Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
 248 1 5 10 15
 250 CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG 213
 251 Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
 252 20 25 30
 254 AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT 261
 255 Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
 256 35 40 45
 258 AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC 309
 259 Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
 260 50 55 60
 262 TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC 357
 263 Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
 264 65 70 75 80
 266 TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT 405
 267 Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
 268 85 90 95
 270 GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA 453
 271 Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
 272 100 105 110
 274 TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC 501
 275 Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
 276 115 120 125
 278 ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT 549
 279 Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
 280 130 135 140
 282 GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT 597
 283 Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala

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284	145	150	155	160	
286	GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG				645
287	Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu				
288	165	170	175		
290	GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT				693
291	Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His				
292	180	185	190		
295	TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC				741
296	Ser Ala Ser Cys Arg Ser Ala Glu Tyr Ser Val His Lys Ile Thr				
297	195	200	205		
299	TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT				789
300	Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn				
301	210	215	220		
303	GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT				837
304	Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe				
305	225	230	235	240	
307	AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA				885
308	Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys				
309	245	250	255		
311	TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC				933
312	Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp				
313	260	265	270		
315	TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC				981
316	Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile				
317	275	280	285		
319	CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC				1029
320	Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly				
321	290	295	300		
323	AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT				1077
324	Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn				
325	305	310	315	320	
327	GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT				1125
328	Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr				
329	325	330	335		
331	CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT				1173
332	Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr				
333	340	345	350		
336	GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC				1221
337	Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala				
338	355	360	365		
340	CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT				1269
341	Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys				
342	370	375	380		
344	CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC				1317
345	Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr				
346	385	390	395	400	
348	AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT				1365
349	Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys				
350	405	410	415		

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:890 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:894 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:898 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:902 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:906 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:914 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:926 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:930 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:950 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:954 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:958 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:962 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:974 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:978 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:982 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:1058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14

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L:1062 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1066 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:1074 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14